

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/575,619
Source: IFWP
Date Processed by STIC: 4/24/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/575,619</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics <input checked="" type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input checked="" type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input checked="" type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input checked="" type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



Suggestion: consult Sequence Rules for valid format

IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/575,619

DATE: 04/24/2006
TIME: 16:32:05

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575619.raw

3 <110> APPLICANT: OSAKA INDUSTRIAL PROMOTION ORGANIZATION
W--> 4 <120> TITLE OF INVENTION: Method for identification polymorphism for
determination illness-risk,
W--> 5 method and array for determination illness-risk
W--> 6 <130> FILE REFERENCE: P04-130
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/575,619
C--> 7 <141> CURRENT FILING DATE: 2006-04-13
7 <150> PRIOR APPLICATION NUMBER: JP 2003-355716
8 <151> PRIOR FILING DATE: 2003-10-15
W--> 9 <160> NUMBER OF SEQ ID: 4
10 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
13 <211> LENGTH: 14
14 <212> TYPE: DNA
15 <213> ORGANISM: Artificial Sequence
W--> 16 <220> FEATURE:
W--> 17 <221> NAME/KEY: Primer
W--> 18 <223> OTHER INFORMATION:
W--> 18 <400> SEQUENCE: 1
E--> 19 ctggagacca ctcccatcct ttct

*see pg 1-2
Does Not Comply
Corrected Diskette Needed*

(14) 24

all explanations

for <213> Artificial Sequence go on

line <223>

They are <223>

*responses, all the
sequences in this
file need to be edited.*

(see p.2)

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2

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> Prove

insert
<223> do you mean probe? \equiv

move to <223> line

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/575,619

DATE: 04/24/2006
TIME: 16:32:06

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575619.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:16 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:18 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:18 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
L:19 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:24 SEQ:1
L:19 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:24 SEQ:1
L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:27 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:27 M:283 W: Missing Blank Line separator, <400> field identifier
L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:27
L:34 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:36 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:36
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:46 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:46